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SEIR MODEL FOR TRANSMISSION OF DENGUE FEVER IN SELANGOR MALAYSIA

SYAFRUDDIN S.

Department of Mathematics, Faculty of Mathematics and Natural Science,
Universitas Negeri Makassar, South Sulawesi, Indonesia
udhinmath_unm@yahoo.com

M. S. M. NOORANI

School of Mathematical Sciences, Universiti Kebangsaan Malaysia,
43600 Bangi, Selangor, Malaysia
msn@ukm.my

In this paper, we study a system of differential equations that models the population dynamics of SEIR vector transmission of dengue fever. The model studied breeding value based on the number of reported cases of dengue fever in Selangor because the state had the highest case in Malaysia. The model explains that maximum level of human infection rate of dengue fever achieved in a very short period. It is also revealed that there existed suitability result between theoretical and empirical calculation using the model. The result of SEIR model will hopefully provide an insight into the spread of dengue fever in Selangor Malaysia and basic form for modeling this area.

Keywords: Dengue fever; endemic; SEIR model; stability; threshold parameter.

1. Introduction

After the Second World War; dengue fever is regarded as a serious infectious disease that risks about 2.5 billion people all over the world, especially in the tropical countries and became a major epidemic disease occurred in Southeast Asia. Such epidemic arises due to climate change and a lack of people knowledge and awareness on dengue fever so that the dengue fever possibly becomes an endemic for a long time. Moreover, World Health Organization (WHO) [26] estimated about 50 to 100 million cases reported. Around 500,000 people are estimated to be infected by hemorrhagic dengue fever each year.

The mathematical models for dengue fever found that compartmental dynamics such as Susceptible, Infected, Removed (SIR) and Susceptible, Exposed, Infected, Removed (SEIR). Particularly, in SIR models [5, 17, 21, 24, 27] and SEIR models [10] had been published. In SIR model exclude the latent period as one of the variables where in SEIR model does count into the latent period as adding vectors variable which examines the spreading of dengue fever. Latent period is very important and crucial because of the

unpredictable climate changing as one of the global warming consequences [1] nowadays.

Hence, in this SEIR model, we constructed and analyzed a mathematical model for its transmission dynamics. The model will apply empirically on data of dengue patients reported by Ministry of Health KKM[a] in Selangor Malaysia (2007) and will be compare to theoretical results which is calculated by ODESOLVE.

1.1. *Dengue fever*

Dengue fever is caused by four serotypes and they are closely related as a family of dengue virus 1 (DEN1), virus 2 (DEN2), virus 3 (DEN3) and virus 4 (DEN4). These viruses carried by two kinds of mosquitoes that are *Aedes aegypti* and *Aedes albopictus* which spread through the mosquitoes bite. According to WHO (2008), *Aedes albopictus* is a kind of mosquito that can transmit the dengue virus and the presence of the species was detected in Asia in recent years. However, *Aedes aegypti* is still the principal vector of dengue virus transmission. Another interesting fact is the shift of patients' phenomena where dengue fever previously attacks children of primary school age, but now everybody is vulnerable to the fever [22].

1.2. *Dengue fever in Selangor Malaysia*

Malaysia is not an exception as one of a country in Southeast Asia from this disease and reflected on the statement that issued by the CDC and the first dengue fever was reported in 1902 [3]. The Spokesman of Ministry of Health said, in 2008, the highest dengue cases in Malaysia is Selangor where 2,391 cases with 5 deaths reported. The cases increase to 103 just in one week compare to previous 2 weeks statistics. Until today, death of dengue Fever has increase to 90 cases and overall is 41034 cases for this year. About 10,318 cases of dengue were reported since January with Kajang reporting the most cases, totaling 1,930. Selangor state government said that so far 32 people have died of dengue fever in the state whereas Kajang recorded only one severe case, Shah Alam and Subang Jaya both reported six deaths [13, 23].

2. SEIR Model

SEIR model is one of a mathematical model to analyze the simulation of the spreading of one serotype of dengue virus between host and vector. The model is based on the Susceptible, Exposed, Infected, Removed (SEIR) of infectious disease epidemiology, which was adopted [10]. SEIR model obtained two vectors, human population (N_h) and Population vector (N_v). Human population (N_h) are divided into four groups, such as people that have the potential to get infected by dengue virus (S_h), people who shows exposed of virus infection (E_h), people who infected (I_h) and people who have recovered (R_h). Population vector or mosquitoes (N_v) are divided into three groups of mosquitoes that potentially infected by dengue virus (S_v), mosquitoes are exposed to infection (E_v) and mosquitoes that were infected with dengue virus (I_v).

In this study, it is assumed that there is numbers of people in the populations that have already infected by the virus while others have not. It is also assumed that the transmission of the virus continues in the population but number of mosquitoes as the vector is constant. People and mosquitoes are categorized in one group at a time. People in the group S_h have a probabilty of being infected with dengue virus at a rate $\frac{\beta_h b I_v}{N_h}$, where $\beta_h b$ is sufficient rate of correlation from human to the vector and count in to the spreading probability from an infected individual to mosquitoes that potentially infected (β_h). In addition, the percentage of infected mosquitoes is (p), average bite of mosquitoes that potentially infected is (b) and the proportional rate for people exposed to dengue virus infection is (φ_h). Once humans infected by dengue virus, they will be given help treatment. Hence, the model assumes that every human being treated will have life time immunity so there will be no re-infection cases. Person's healing rate from a virus infection stipulated from a given treatment or the duration of infection in the body is proportional to the individual (γ_h).

Changes for the group S_v show that each has a probability of mosquitoes infected with dengue virus at a rate $\left(\frac{\beta_v b I_h}{N_h}\right)$, where $\beta_v b = \gamma_v$ is sufficient rate of correlation from vectors to humans and count in to the probability of transmission from infected mosquitoes to the potentially infected human (β_v). In addition, average bite of an infected mosquitoes is (b), the proportional rates of mosquitoes exposed to the virus infection is (δ_v). Both group of people and mosquitoes will be reduced due to natural death, symbolized with (μ_h) and (μ_v) respectively. For the people who have infected, there is a death caused by dengue itself with the content (α_h). Changes that occur in every group of people and mosquitoes can be defined as the following mathematical model

Human Population

$$\frac{dS_h}{dt} = \mu_h N_h - \left(\frac{\beta_h b I_v}{N_h} + p + \mu_h\right) S_h \tag{1}$$

$$\frac{dE_h}{dt} = \left(\frac{\beta_h b I_v}{N_h} + p\right) S_h - (\mu_h + \varphi_h) E_h \tag{2}$$

$$\frac{dI_h}{dt} = \varphi_h E_h - (\mu_h + \gamma_h + \alpha_h) I_h \tag{3}$$

$$\frac{dR_h}{dt} = \gamma_h I_h - \mu_h R_h \tag{4}$$

Vector Population

$$\frac{dS_v}{dt} = A - \left(\frac{\beta_v b I_h}{N_h} + \mu_v\right) S_v \tag{5}$$

$$\frac{dE_v}{dt} = \frac{\beta_v b I_h}{N_h} S_v - (\mu_v + \delta_v) E_v \tag{6}$$

$$\frac{dI_v}{dt} = \delta_v E_v - \mu_v I_v \tag{7}$$

with condition;

$$N_h = S_h + E_h + I_h + R_h \Rightarrow R_h = N_h - S_h - E_h - I_h \tag{8}$$

$$N_v = \frac{A}{\mu_v} = S_v + E_v + I_v \Rightarrow S_v = \frac{A}{\mu_v} - E_v - I_v \tag{9}$$

Thus, the model for the human and mosquito populations can be simplified as follows;

$$\frac{dS_h}{dt} = \mu_h N_h - \left(\frac{\beta_h b I_v}{N_h} + p + \mu_h\right) S_h \tag{10}$$

$$\frac{dE_h}{dt} = \left(\frac{\beta_h b I_v}{N_h} + p\right) S_h - (\mu_h + \varphi_h) E_h \tag{11}$$

$$\frac{dI_h}{dt} = \varphi_h E_h - (\mu_h + \gamma_h + \alpha_h) I_h \tag{12}$$

$$\frac{dE_v}{dt} = \frac{\beta_v b I_h}{N_h} S_v - (\mu_v + \delta_v) E_v \tag{13}$$

$$\frac{dI_v}{dt} = \delta_v E_v - \mu_v I_v \tag{14}$$

The model can be simplified by assuming the following fractions,

$$x = \frac{S_h}{N_h}, u = \frac{E_h}{N_h}, y = \frac{I_h}{N_h}, w = \frac{E_v}{N_v} \text{ and } z = \frac{I_v}{N_v} = \frac{I_v}{A/\mu_v} \tag{15}$$

Thus, the model for the human and mosquito populations can be simplified as follows;

$$\frac{dx}{dt} = \mu_h(1 - x) - px - \alpha xz$$
$$\frac{du}{dt} = (\alpha z + p)x - (\mu_h + \varphi_h)u$$
$$\frac{dy}{dt} = \varphi_h u - (\mu_h + \gamma_h + \alpha_h)y$$
$$\frac{dw}{dt} = \gamma_v(1 - z - w)y - (\mu_v + \delta_v)w$$
$$\frac{dz}{dt} = \delta_v w - \mu_v z \tag{16}$$

with value $\alpha = \frac{\beta_h bA}{N_h \mu_v}$

2.1. *Equilibrium point for SEIR model in Selangor Malaysia*

Parameters in this model are variously determined. Some of the parameter values is taken from the Annual Health Facts by KKM[a] in 2007, as well as from previous studies (Derouich & Boutayeb 2006) due to lack of information in the KKM[a] data. In addition, the model also used parameter values from Singapore. Lee Han Lim (2009) study stated that infection rate of the mosquitoes population is around 10%. According to Lee (2000), life expectancy for the female *Aedes aegypti* is between 12 to 56 days and the average was 34 days, as well as KC Ang & Z. Li (1999) study stated that percentage of mosquitoes are infected (p) and the rate for people exposed to dengue virus infection is proportional (φ_h). The study on Singapore cases were used in this model because Singapore and Malaysia are neighbors hence both countries have a similar environment and climate, then the value of the parameter estimates for mosquito infection rates in Malaysia are similar. Next table shows parameters, values and sources of parameter.

Table 1. Parameter values.

Parameter	Value	Sources
μ_h	0.0045000	(KKM 2007)
γ_h	0.3288330	(KKM 2007)
α_h	0.0000002	(KKM 2007)
$\beta_v b$	0.3750000	(Derouich & Boutayeb 2006)
$\beta_h b$	0.7500000	(Derouich & Boutayeb 2006)
μ_v	0.02941000	(Lee Han Lin 2000)
p	0.0900000	(K.C. Ang & Z. Li 1999)
φ_h	0.1667000	(K.C. Ang & Z. Li 1999)
δ_v	0.1428000	(KKM 2007)

Critical point will occur while the value of $\frac{dx}{dt} = \frac{du}{dt} = \frac{dy}{dt} = \frac{dw}{dt} = \frac{dz}{dt} = 0$ and eequilibrium point is determined using a set of SEIR model with parameters in Selangor has been set. Then, to determine the critical point, Eq. (16) is set equal to zero, as shown below:

$$0.0045(1 - x) - 0.09x - 0.006xz = 0 \tag{17}$$

$$0.006xz + 0.09x - (0.1667 + 0.0045)u = 0 \qquad (18)$$

$$0.1667u - (0.328833 + 0.0045 + 0.0000002)y = 0 \qquad (19)$$

$$0.375(1 - z - w)y - (0.02941 + 0.1428)w = 0 \qquad (20)$$

$$0.1428w - 0.02941z = 0 \qquad (21)$$

By using the software MAPLE obtained equilibrium points as follows:

$(x, u, y, w, z) = (6.665956, -0.14893, -0.074476, -3.220572, -15.637488)$ and $(0.0047276, 0.025042, 0.012524, 0.023516, 0.114182)$.

The equilibrium points $(6.665956, -0.14893, -0.074476, -3.220572, -15.637488)$ is not suitable to be studied because only the value of S_h is positive while other value is negative and it is illogical.

Eigen values λ for Eq. (16) are the equilibrium point $(6.665956, -0.14893, -0.074476, -3.220572, -15.637488)$ is obtained *eigen* values: $\lambda = -0.169104 + 0.266988i$, $\lambda = -0.169104 - 0.266988i$, $\lambda = -0.483472$, $\lambda = 0.147266$ and $\lambda = -0.004485$ and the equilibrium point $(0.0047276, 0.025042, 0.012524, 0.023516, 0.114182)$ is obtained *eigen* values: $\lambda = -0.17252 + 0.014402i$, $\lambda = -0.17252 - 0.014402i$, $\lambda = -0.333716$, $\lambda = -0.092982$ and $\lambda = -0.034296$.

Stability of SEIR model to the analysis based on each point of equilibrium is obtained. The results of the model solution in search of equilibrium points and *eigen* values λ are shown in Table 2.

Table 2. Equilibrium points and stability analysis.

Equilibrium points $(S_h, E_h, I_h, E_v, I_v)$	Eigen values, λ	Stability analysis
(0.0047276, 0.025042, 0.012524, 0.023516, 0.114182)	Compleks and all negative signs	Focus stable asymptotic

Referring to the equilibrium points that were obtained, the equilibrium points $(0.0047276, 0.025042, 0.012524, 0.023516, 0.114182)$ for the state of Selangor are the focus of equilibrium points which asymptotically stable. It shows that if the number of people whom potentially infected at a rate of 0.0047276, the number of people who are exposed at a rate of 0.025042 and the number of people who get infected at a rate of 0.012524 of the human population.

The stability analysis of SEIR model explains the dengue fever is asymptotically stable and focused on several areas in the state Selangor. Our model shows that dengue fever is not significant in this area.

3. Result and Discussion

3.1. *Numerical result of SEIR model in Selangor Malaysia*

Numerical solution is presented for the transmission of dengue fever in Selangor. Data on the number of dengue fever cases in the state of Selangor, Malaysia (Figure 1) and the results of SEIR model for the state of Selangor is described in Figure 2 with the x-axis is the time (in months) and the y-axis is the fraction of the variables used.
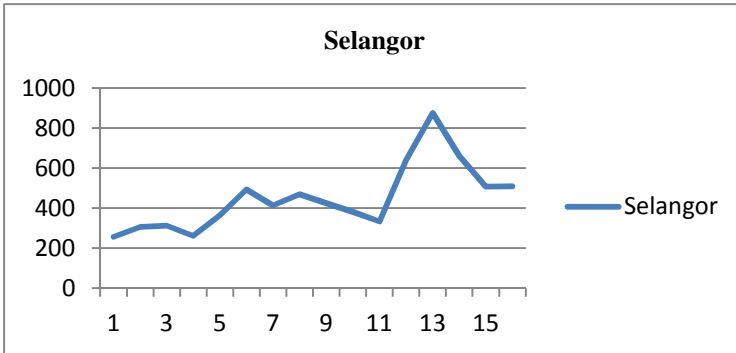
Fig. 1. Number of cases reported in Selangor Malaysia and Sulawesi Selatan in 2008 on a monthly basis.

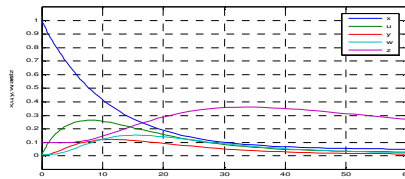Result of SEIR model simulation for the state of Selangor by using MATLAB

Fig. 2. Transmission of dengue fever with initial condition $S_h(0) = \frac{5070822}{5071126}$, $E_h(0) = \frac{50711}{5071126}$, $I_h(0) = \frac{304}{5071126}$ $E_v(0) = 0.01$ and $I_v(0) = 0.1$ with parameter $\mu_h = 0.0045$, $p = 0.09$, $C_{vh} = 0.75$, $\varphi_h = 0.1667$ $C_{hv} = 0.375$, $\delta_v = 0.1428$ $\alpha_h = 0.0000002$, $\gamma_h = 0.328833$ and $\mu_v = 0.02941$.

According to Figure 1 and Figure 2, the number of dengue fever cases (virus infected people) shows that number of virus infection will reach the highest level (12%) of the human population after 13th month and the number of people infected will be reduced close to zero for the next 32th month. In addition, the number of people exposed reach the peak level at the 8th month and then will fall close to zero for the next 32th month. The results produce by appropriate parameter used in the model, meanwhile, the number of infected mosquitoes in Figure 2 takes about for the next 33th month to achieve the highest total for almost 40% of the population of mosquitoes. In addition, the number of infected mosquito takes more than 60 months to approach zero point. This indication means that the mosquito population to take more to diminish.

Simulation using SEIR model for dengue fever cases in Selangor Malaysia also reveal that the total of reported cases during 2008 had not reached a serious level. Reported cases of dengue fever were as high as 12% of the total population of 5.071126 people in Selangor, Malaysia. Suitability graph of SEIR Model and real data for Dengue Fever in Selangor Malaysia can see in Figure 3.
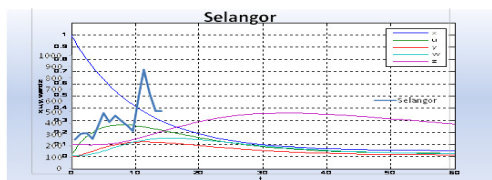

Fig. 3. Graph of SEIR model and real data in Selangor Malaysia

3.2. *Breeding rates,* R_0

Searching for the re-breeding rates R_0 is important because it shows how many infections will occur to individuals as a result of an infection. If an infection can infect others for more than one, so the value $R_0 > 1$ and dengue fever become epidemic. Determination of the reproduction rate has been introduced by [18]. The basis for determining value R_0 is use to prevail the infection rate to individuals who have the potential to be infected $\left(\frac{b\beta_v I_v}{N_h} \right)$ and rates for individuals who have recovered (γ_h).

Simulation carried out using ODESOLVE, MATLAB. Stability analysis was carried out for the epidemic and values of the threshold were obtained. Illustration of the dynamics of each epidemic is given in Figure 4 and Figure 5.
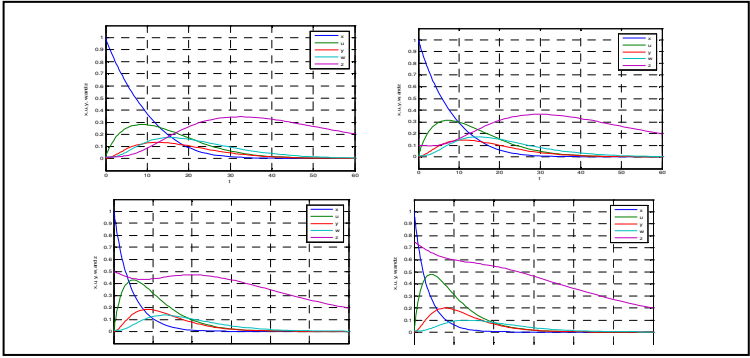

Fig. 4. Illustration of the dynamics system with $R_0 \leq 1$ (Convergence)

Figure 4 shows the typical behavior of the solutions indicating the rate of Susceptible, Exposed, Infectious and Removed approaches asymptotically, the trivial state of the system (the ideal state) to the case where all the population is will remain healthy.
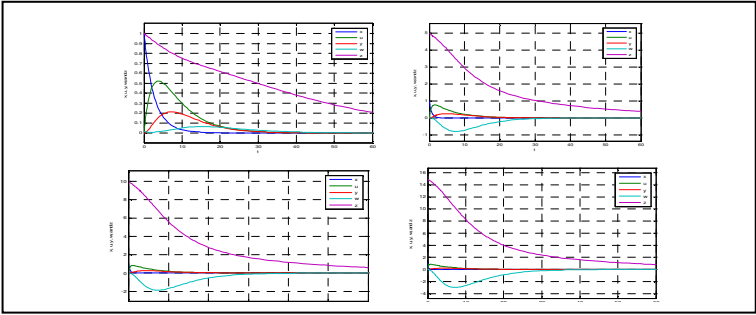

Fig. 5. Illustration of the dynamics system with $R_0 > 1$ (Oscillation)

Figure 5 illustrates an oscillatory behavior near the neighborhood of the endemic equilibrium point. This behavior can be justified by the fact that if $R_0 > 1$ and if the initial value I_h satisfy the solution.

By using the initial values and parameter values from data in Selangor then obtained result of threshold parameter value R_0 for Selangor can be rewritten in mathematical form as follows:

$$R_0 = \frac{(C_{hv} I_v)/N_h}{\gamma_h} S(0) = 1.1403 \, I_v$$

The reproductive rates depend on the number of infected mosquitoes (I_v). Determination of value R_0 is accomplished by replacing I_v to some of the different values shown in Table 3. The difference between these values I_v is very significant.

Table 3. Determination of the reproductive value R_0 of infected mosquitoes.

I_v value	R_0 value
0.056	0.0639
0.1	0.11403
0.5	0.5702
0.75	0.8552
1	1.1403
5	5.7015
10	11.403

Table 3 shows, if the number of infected mosquitoes less than one, $I_v < 1$ then the value $R_0 < 1$. These values $I_v = 0.056$ and $I_v = 0.1$ reflect the case in Selangor, Malaysia. Thus, cases of dengue fever in the state of Selangor is not significant, because the results obtained show that the dengue virus infection is low because an individual who get infected will cause less infection to the others that have potential to infect others. If the number of mosquitoes infected more than one $I_v > 1$, then the value $R_0 > 1$. Corollary, the spreading of dengue virus causes more than one person infected by dengue virus.

4. Conclusion

Result of the SEIR model indicates that infection to human based on real data in Selangor is not harmful yet and underline that maximum level of human infection rate of dengue fever achieved in a very short period.

Dengue fever takes very long time to ensure that the number of infected people in zero values. This is due to dengue virus infection occurs when there is a continuous correlation between human and mosquito population. Mosquitoes are the carriers that can cause a virus infection to human. Furthermore, the empirical SEIR model produce similar result to the theoretical model and described that the latent period variable significantly explain the transmission of dengue fever.

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